CRF Errors Corrected by the STIC Systems Branch

Serial Number: 09/446,415B

CRF Processing Date: 6-3-02
Edited by: M. SPENCER
Verified by: _____ (STIC sta

1631

ENTERED

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line

☐ Edited a format error in the Current Application Data section, specifically:

_____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:

_____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

_____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

_____

TECH CENTER 1600/2900
RECEIVED JUN 0 6 2002
#16

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included:

_____

☐ Deleted extra, invalid, headings used by an applicant, specifically:

_____

☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as_____.

☑ Inserted mandatory headings, specifically: <220> SEQ ID #2

☐ Corrected an obvious error in the response, specifically:

_____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:

_____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☐ Other:

_____
_____
_____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

1600

```
RAW SEQUENCE LISTING             DATE: 06/03/2002
PATENT APPLICATION:  US/09/446,415B    TIME: 10:54:04

         Input Set : A:\ptoms.txt
         Output Set: N:\CRF3\06032002\I446415B.raw

 3 <110> APPLICANT: Beamer, Lesa J.
 4         Eisenberg, David
 5         Carroll, Stephen F.
 7 <120> TITLE OF INVENTION: BACTERICIDAL/PERMEABILITY-INCREASING PROTEIN:
 8         CRYSTALLIZATION, X-RAY DIFFRACTION, THREE-DIMENSIONAL
 9         STRUCTURE DETERMINATION, RATIONAL DRUG DESIGN AND
10         MOLECULAR MODELING OF RELATED PROTEINS
12 <130> FILE REFERENCE: 11034US02
14 <140> CURRENT APPLICATION NUMBER: 09/446,415B
15 <141> CURRENT FILING DATE: 2000-07-19
17 <150> PRIOR APPLICATION NUMBER: 08/879,565
18 <151> PRIOR FILING DATE: 1997-06-20
20 <160> NUMBER OF SEQ ID NOS: 12
22 <170> SOFTWARE: PatentIn Ver. 2.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1813
26 <212> TYPE: DNA
27 <213> ORGANISM: Human
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (31)..(1491)
33 <220> FEATURE:
34 <221> NAME/KEY: mat_peptide
35 <222> LOCATION: (124)..(1491)
37 <220> FEATURE:
38 <223> OTHER INFORMATION: "rBPI"
40 <400> SEQUENCE: 1
41 caggccttga ggttttggca gctctggagg atg aga gag aac atg gcc agg ggc   54
42                                   Met Arg Glu Asn Met Ala Arg Gly
43                                   -30             -25
45 cct tgc aac gcg ccg aga tgg gtg tcc ctg atg gtg ctc gtc gcc ata  102
46 Pro Cys Asn Ala Pro Arg Trp Val Ser Leu Met Val Leu Val Ala Ile
47             -20             -15             -10
49 ggc acc gcc gtg aca gcg gcc gtc aac cct ggc gtc gtg gtc agg atc  150
50 Gly Thr Ala Val Thr Ala Ala Val Asn Pro Gly Val Val Val Arg Ile
51          -5             -1  1               5
53 tcc cag aag ggc ctg gac tac gcc agc cag cag ggg acg gcc gct ctg  198
54 Ser Gln Lys Gly Leu Asp Tyr Ala Ser Gln Gln Gly Thr Ala Ala Leu
55   10              15              20              25
57 cag aag gag ctg aag agg atc aag att cct gac tac tca gac agc ttt  246
58 Gln Lys Glu Leu Lys Arg Ile Lys Ile Pro Asp Tyr Ser Asp Ser Phe
59             30              35              40
61 aag atc aag cat ctt ggg aag ggg cat tat agc ttc tac agc atg gac  294
```

```
62 Lys Ile Lys His Leu Gly Lys Gly His Tyr Ser Phe Tyr Ser Met Asp
63             45                  50                  55
65 atc cgt gaa ttc cag ctt ccc agt tcc cag ata agc atg gtg ccc aat    342
66 Ile Arg Glu Phe Gln Leu Pro Ser Ser Gln Ile Ser Met Val Pro Asn
67         60                  65                  70
69 gtg ggc ctt aag ttc tcc atc agc aac gcc aat atc aag atc agc ggg    390
70 Val Gly Leu Lys Phe Ser Ile Ser Asn Ala Asn Ile Lys Ile Ser Gly
71     75                  80                  85
73 aaa tgg aag gca caa aag aga ttc tta aaa atg agc ggc aat ttt gac    438
74 Lys Trp Lys Ala Gln Lys Arg Phe Leu Lys Met Ser Gly Asn Phe Asp
75 90                  95                  100                 105
77 ctg agc ata gaa ggc atg tcc att tcg gct gat ctg aag ctg ggc agt    486
78 Leu Ser Ile Glu Gly Met Ser Ile Ser Ala Asp Leu Lys Leu Gly Ser
79             110                 115                 120
81 aac ccc acg tca ggc aag ccc acc atc acc tgc tcc agc tgc agc agc    534
82 Asn Pro Thr Ser Gly Lys Pro Thr Ile Thr Cys Ser Ser Cys Ser Ser
83             125                 130                 135
85 cac atc aac agt gtc cac gtg cac atc tca aag agc aaa gtc ggg tgg    582
86 His Ile Asn Ser Val His Val His Ile Ser Lys Ser Lys Val Gly Trp
87         140                 145                 150
89 ctg atc caa ctc ttc cac aaa aaa att gag tct gcg ctt cga aac aag    630
90 Leu Ile Gln Leu Phe His Lys Lys Ile Glu Ser Ala Leu Arg Asn Lys
91     155                 160                 165
93 atg aac agc cag gtc tgc gag aaa gtg acc aat tct gta tcc tcc aag    678
94 Met Asn Ser Gln Val Cys Glu Lys Val Thr Asn Ser Val Ser Ser Lys
95 170                 175                 180                 185
97 ctg caa cct tat ttc cag act ctg cca gta atg acc aaa ata gat tct    726
98 Leu Gln Pro Tyr Phe Gln Thr Leu Pro Val Met Thr Lys Ile Asp Ser
99             190                 195                 200
101 gtg gct gga atc aac tat ggt ctg gtg gca cct cca gca acc acg gct    774
102 Val Ala Gly Ile Asn Tyr Gly Leu Val Ala Pro Pro Ala Thr Thr Ala
103             205                 210                 215
105 gag acc ctg gat gta cag atg aag ggg gag ttt tac agt gag aac cac    822
106 Glu Thr Leu Asp Val Gln Met Lys Gly Glu Phe Tyr Ser Glu Asn His
107         220                 225                 230
109 cac aat cca cct ccc ttt gct cca cca gtg atg gag ttt ccc gct gcc    870
110 His Asn Pro Pro Pro Phe Ala Pro Pro Val Met Glu Phe Pro Ala Ala
111     235                 240                 245
113 cat gac cgc atg gta tac ctg ggc ctc tca gac tac ttc ttc aac aca    918
114 His Asp Arg Met Val Tyr Leu Gly Leu Ser Asp Tyr Phe Phe Asn Thr
115 250                 255                 260                 265
117 gcc ggg ctt gta tac caa gag gct ggg gtc ttg aag atg acc ctt aga    966
118 Ala Gly Leu Val Tyr Gln Glu Ala Gly Val Leu Lys Met Thr Leu Arg
119             270                 275                 280
121 gat gac atg att cca aag gag tcc aaa ttt cga ctg aca acc aag ttc   1014
122 Asp Asp Met Ile Pro Lys Glu Ser Lys Phe Arg Leu Thr Thr Lys Phe
123             285                 290                 295
125 ttt gga acc ttc cta cct gag gtg gcc aag aag ttt ccc aac atg aag   1062
126 Phe Gly Thr Phe Leu Pro Glu Val Ala Lys Lys Phe Pro Asn Met Lys
```

RAW SEQUENCE LISTING   DATE: 06/03/2002
PATENT APPLICATION: US/09/446,415B   TIME: 10:54:04

Input Set : A:\ptoms.txt
Output Set: N:\CRF3\06032002\I446415B.raw

```
127        300                305                310
129 ata cag atc cat gtc tca gcc tcc acc ccg cca cac ctg tct gtg cag    1110
130 Ile Gln Ile His Val Ser Ala Ser Thr Pro Pro His Leu Ser Val Gln
131        315                320                325
133 ccc acc ggc ctt acc ttc tac cct gcc gtg gat gtc cag gcc ttt gcc    1158
134 Pro Thr Gly Leu Thr Phe Tyr Pro Ala Val Asp Val Gln Ala Phe Ala
135 330                335                340                345
137 gtc ctc ccc aac tcc tcc ctg gct tcc ctc ttc ctg att ggc atg cac    1206
138 Val Leu Pro Asn Ser Ser Leu Ala Ser Leu Phe Leu Ile Gly Met His
139                350                355                360
141 aca act ggt tcc atg gag gtc agc gcc gag tcc aac agg ctt gtt gga    1254
142 Thr Thr Gly Ser Met Glu Val Ser Ala Glu Ser Asn Arg Leu Val Gly
143                365                370                375
145 gag ctc aag ctg gat agg ctg ctc ctg gaa ctg aag cac tca aat att    1302
146 Glu Leu Lys Leu Asp Arg Leu Leu Leu Glu Leu Lys His Ser Asn Ile
147        380                385                390
149 ggc ccc ttc ccg gtt gaa ttg ctg cag gat atc atg aac tac att gta    1350
150 Gly Pro Phe Pro Val Glu Leu Leu Gln Asp Ile Met Asn Tyr Ile Val
151        395                400                405
153 ccc att ctt gtg ctg ccc agg gtt aac gag aaa cta cag aaa ggc ttc    1398
154 Pro Ile Leu Val Leu Pro Arg Val Asn Glu Lys Leu Gln Lys Gly Phe
155 410                415                420                425
157 cct ctc ccg acg ccg gcc aga gtc cag ctc tac aac gta gtg ctt cag    1446
158 Pro Leu Pro Thr Pro Ala Arg Val Gln Leu Tyr Asn Val Val Leu Gln
159                430                435                440
161 cct cac cag aac ttc ctg ctg ttc ggt gca gac gtt gtc tat aaa        1491
162 Pro His Gln Asn Phe Leu Leu Phe Gly Ala Asp Val Val Tyr Lys
163                445                450                455
165 tgaaggcacc aggggtgccg ggggctgtca gccgcacctg ttcctgatgg gctgtggggc 1551
167 accggctgcc tttccccagg gaatcctctc cagatcttaa ccaagagccc cttgcaaact 1611
169 tcttcgactc agattcagaa atgatctaaa cacgaggaaa cattattcat tggaaaagtg 1671
171 catggtgtgt attttaggga ttatgagctt ctttcaaggg ctaaggctgc agagatattt 1731
173 cctccaggaa tcgtgtttca attgtaacca agaaatttcc atttgtgctt catgaaaaaa 1791
175 aacttctggt tttttcatg tg                                            1813
178 <210> SEQ ID NO: 2
179 <211> LENGTH: 487
180 <212> TYPE: PRT
181 <213> ORGANISM: Human
182 <220> FEATURE:          W-->
183 <223> OTHER INFORMATION: "rBPI"
185 <400> SEQUENCE: 2
186 Met Arg Glu Asn Met Ala Arg Gly Pro Cys Asn Ala Pro Arg Trp Val
187        -30                -25                -20
189 Ser Leu Met Val Leu Val Ala Ile Gly Thr Ala Val Thr Ala Ala Val
190 -15                -10                -5                 -1  1
192 Asn Pro Gly Val Val Val Arg Ile Ser Gln Lys Gly Leu Asp Tyr Ala
193                5                10                 15
195 Ser Gln Gln Gly Thr Ala Ala Leu Gln Lys Glu Leu Lys Arg Ile Lys
196        20                25                30
```

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198 Ile Pro Asp Tyr Ser Asp Ser Phe Lys Ile Lys His Leu Gly Lys Gly
199      35              40                 45
201 His Tyr Ser Phe Tyr Ser Met Asp Ile Arg Glu Phe Gln Leu Pro Ser
202  50              55                 60                    65
204 Ser Gln Ile Ser Met Val Pro Asn Val Gly Leu Lys Phe Ser Ile Ser
205              70                 75                 80
207 Asn Ala Asn Ile Lys Ile Ser Gly Lys Trp Lys Ala Gln Lys Arg Phe
208          85                 90                    95
210 Leu Lys Met Ser Gly Asn Phe Asp Leu Ser Ile Glu Gly Met Ser Ile
211         100                105                110
213 Ser Ala Asp Leu Lys Leu Gly Ser Asn Pro Thr Ser Gly Lys Pro Thr
214     115                120                125
216 Ile Thr Cys Ser Ser Cys Ser Ser His Ile Asn Ser Val His Val His
217 130                135                140                    145
219 Ile Ser Lys Ser Lys Val Gly Trp Leu Ile Gln Leu Phe His Lys Lys
220             150                155                160
222 Ile Glu Ser Ala Leu Arg Asn Lys Met Asn Ser Gln Val Cys Glu Lys
223             165                170                175
225 Val Thr Asn Ser Val Ser Ser Lys Leu Gln Pro Tyr Phe Gln Thr Leu
226     180                185                190
228 Pro Val Met Thr Lys Ile Asp Ser Val Ala Gly Ile Asn Tyr Gly Leu
229     195                200                205
231 Val Ala Pro Pro Ala Thr Thr Ala Glu Thr Leu Asp Val Gln Met Lys
232 210                215                220                    225
234 Gly Glu Phe Tyr Ser Glu Asn His His Asn Pro Pro Pro Phe Ala Pro
235             230                235                240
237 Pro Val Met Glu Phe Pro Ala Ala His Asp Arg Met Val Tyr Leu Gly
238             245                250                255
240 Leu Ser Asp Tyr Phe Phe Asn Thr Ala Gly Leu Val Tyr Gln Glu Ala
241         260                265                270
243 Gly Val Leu Lys Met Thr Leu Arg Asp Asp Met Ile Pro Lys Glu Ser
244     275                280                285
246 Lys Phe Arg Leu Thr Thr Lys Phe Phe Gly Thr Phe Leu Pro Glu Val
247 290                295                300                    305
249 Ala Lys Lys Phe Pro Asn Met Lys Ile Gln Ile His Val Ser Ala Ser
250             310                315                320
252 Thr Pro Pro His Leu Ser Val Gln Pro Thr Gly Leu Thr Phe Tyr Pro
253         325                330                335
255 Ala Val Asp Val Gln Ala Phe Ala Val Leu Pro Asn Ser Ser Leu Ala
256         340                345                350
258 Ser Leu Phe Leu Ile Gly Met His Thr Thr Gly Ser Met Glu Val Ser
259     355                360                365
261 Ala Glu Ser Asn Arg Leu Val Gly Glu Leu Lys Leu Asp Arg Leu Leu
262 370                375                380                    385
264 Leu Glu Leu Lys His Ser Asn Ile Gly Pro Phe Pro Val Glu Leu Leu
265             390                395                400
267 Gln Asp Ile Met Asn Tyr Ile Val Pro Ile Leu Val Leu Pro Arg Val
268         405                410                415
270 Asn Glu Lys Leu Gln Lys Gly Phe Pro Leu Pro Thr Pro Ala Arg Val
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RAW SEQUENCE LISTING   DATE: 06/03/2002
PATENT APPLICATION: US/09/446,415B   TIME: 10:54:04

Input Set : A:\ptoms.txt
Output Set: N:\CRF3\06032002\I446415B.raw

```
271        420          .        425               430
273 Gln Leu Tyr Asn Val Val Leu Gln Pro His Gln Asn Phe Leu Leu Phe
274     435               440               445
276 Gly Ala Asp Val Val Tyr Lys
277 450               455
281 <210> SEQ ID NO: 3
282 <211> LENGTH: 456
283 <212> TYPE: PRT
284 <213> ORGANISM: Human
286 <220> FEATURE:
287 <223> OTHER INFORMATION: bactericidal/permeability-increasing protein (BPI)
288      (Figure 5)
290 <400> SEQUENCE: 3
291 Val Asn Pro Gly Val Val Val Arg Ile Ser Gln Lys Gly Leu Asp Tyr
292   1             5               10              15
294 Ala Ser Gln Gln Gly Thr Ala Ala Leu Gln Lys Glu Leu Lys Arg Ile
295            20               25               30
297 Lys Ile Pro Asp Tyr Ser Asp Ser Phe Lys Ile Lys His Leu Gly Lys
298         35               40               45
300 Gly His Tyr Ser Phe Tyr Ser Met Asp Ile Arg Glu Phe Gln Leu Pro
301      50               55               60
303 Ser Ser Gln Ile Ser Met Val Pro Asn Val Gly Leu Lys Phe Ser Ile
304 65          .       70               75              80
306 Ser Asn Ala Asn Ile Lys Ile Ser Gly Lys Trp Lys Ala Gln Lys Arg
307   .             85               90               95
309 Phe Leu Lys Met Ser Gly Asn Phe Asp Leu Ser Ile Glu Gly Met Ser
310            100              105              110
312 Ile Ser Ala Asp Leu Lys Leu Gly Ser Asn Pro Thr Ser Gly Lys Pro
313         115              120              125
315 Thr Ile Thr Cys Ser Ser Cys Ser Ser His Ile Asn Ser Val His Val
316      130              135              140
318 His Ile Ser Lys Ser Lys Val Gly Trp Leu Ile Gln Leu Phe His Lys
319 145              150              155              160
321 Lys Ile Glu Ser Ala Leu Arg Asn Lys Met Asn Ser Gln Val Cys Glu
322            165              170              175
324 Lys Val Thr Asn Ser Val Ser Ser Glu Leu Gln Pro Tyr Phe Gln Thr
325         180              185              190
327 Leu Pro Val Met Thr Lys Ile Asp Ser Val Ala Gly Ile Asn Tyr Gly
328         195              200              205
330 Leu Val Ala Pro Pro Ala Thr Thr Ala Glu Thr Leu Asp Val Gln Met
331      210              215              220
333 Lys Gly Glu Phe Tyr Ser Glu Asn His His Asn Pro Pro Pro Phe Ala
334 225              230              235              240
336 Pro Pro Val Met Glu Phe Pro Ala Ala His Asp Arg Met Val Tyr Leu
337            245              250              255
339 Gly Leu Ser Asp Tyr Phe Phe Asn Thr Ala Gly Leu Val Tyr Gln Glu
340            260              265              270
342 Ala Gly Val Leu Lys Met Thr Leu Arg Asp Asp Met Ile Pro Lys Glu
343         275              280              285
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VERIFICATION SUMMARY   DATE: 06/03/2002
PATENT APPLICATION: US/09/446,415B   TIME: 10:54:05

Input Set : A:\ptoms.txt
Output Set: N:\CRF3\06032002\I446415B.raw

L:182 M:283 W: Missing Blank Line separator, <220> field identifier

Does Not Comply
Corrected Diskette Needed

1600

RAW SEQUENCE LISTING   DATE: 05/23/2002
PATENT APPLICATION: US/09/446,415B   TIME: 17:01:31

Input Set : A:\11034US02.SEQ.txt
Output Set: N:\CRF3\05232002\I446415B.raw

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   3 <110> APPLICANT: Beamer, Lesa J.
   4         Eisenberg, David
   5         Carroll, Stephen F.
   7 <120> TITLE OF INVENTION: BACTERICIDAL/PERMEABILITY-INCREASING PROTEIN:
   8         CRYSTALLIZATION, X-RAY DIFFRACTION, THREE-DIMENSIONAL
   9         STRUCTURE DETERMINATION, RATIONAL DRUG DESIGN AND
  10         MOLECULAR MODELING OF RELATED PROTEINS
  12 <130> FILE REFERENCE: 11034US02
  14 <140> CURRENT APPLICATION NUMBER: 09/446,415B
  15 <141> CURRENT FILING DATE: 2000-07-19
  17 <150> PRIOR APPLICATION NUMBER: 08/879,565
  18 <151> PRIOR FILING DATE: 1997-06-20
  20 <160> NUMBER OF SEQ ID NOS: 12
  22 <170> SOFTWARE: PatentIn Ver. 2.1
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ERRORED SEQUENCES

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 178 <210> SEQ ID NO: 2
 179 <211> LENGTH: 487
 180 <212> TYPE: PRT
 181 <213> ORGANISM: Human
 182 <223> OTHER INFORMATION: "rBPI"
E--> 184 <400> SEQUENCE: 2
 185 Met Arg Glu Asn Met Ala Arg Gly Pro Cys Asn Ala Pro Arg Trp Val
 186      -30                 -25                 -20
 188 Ser Leu Met Val Leu Val Ala Ile Gly Thr Ala Val Thr Ala Ala Val
 189 -15               -10                 -5                 -1  1
 191 Asn Pro Gly Val Val Val Arg Ile Ser Gln Lys Gly Leu Asp Tyr Ala
 192              5                 10                 15
 194 Ser Gln Gln Gly Thr Ala Ala Leu Gln Lys Glu Leu Lys Arg Ile Lys
 195          20                 25                 30
 197 Ile Pro Asp Tyr Ser Asp Ser Phe Lys Ile Lys His Leu Gly Lys Gly
 198      35                 40                 45
 200 His Tyr Ser Phe Tyr Ser Met Asp Ile Arg Glu Phe Gln Leu Pro Ser
 201 50                 55                 60                 65
 203 Ser Gln Ile Ser Met Val Pro Asn Val Gly Leu Lys Phe Ser Ile Ser
 204              70                 75                 80
 206 Asn Ala Asn Ile Lys Ile Ser Gly Lys Trp Lys Ala Gln Lys Arg Phe
 207          85                 90                 95
 209 Leu Lys Met Ser Gly Asn Phe Asp Leu Ser Ile Glu Gly Met Ser Ile
 210      100               105                110
 212 Ser Ala Asp Leu Lys Leu Gly Ser Asn Pro Thr Ser Gly Lys Pro Thr
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[handwritten annotation]: mandatory numeric identifier, <220>, missing.

RAW SEQUENCE LISTING   DATE: 05/23/2002
PATENT APPLICATION: US/09/446,415B   TIME: 17:01:31

Input Set : A:\11034US02.SEQ.txt
Output Set: N:\CRF3\05232002\I446415B.raw

```
213     115                 120                 125
215 Ile Thr Cys Ser Ser Cys Ser Ser His Ile Asn Ser Val His Val His
216 130                 135                 140                 145
218 Ile Ser Lys Ser Lys Val Gly Trp Leu Ile Gln Leu Phe His Lys Lys
219         ·       150·                155                 160
221 Ile Glu Ser Ala Leu Arg Asn Lys Met Asn Ser Gln Val Cys Glu Lys
222             165                 170                 175
224 Val Thr Asn Ser Val Ser Ser Lys Leu Gln Pro Tyr Phe Gln Thr Leu
225             180                 185                 190
227 Pro Val Met Thr Lys Ile Asp Ser Val Ala Gly Ile Asn Tyr Gly Leu
228         195                 200                 205
230 Val Ala Pro Pro Ala Thr Thr Ala Glu Thr Leu Asp Val Gln Met Lys
231 210                 215                 220                 225
233 Gly Glu Phe Tyr Ser Glu Asn His His Asn Pro Pro Pro Phe Ala Pro
234             230                 235                 240
236 Pro Val Met Glu Phe Pro Ala Ala His Asp Arg Met Val Tyr Leu Gly
237             245                 250                 255
239 Leu Ser Asp Tyr Phe Phe Asn Thr Ala Gly Leu Val Tyr Gln Glu Ala
240             260                 265                 270
242 Gly Val Leu Lys Met Thr Leu Arg Asp Asp Met Ile Pro Lys Glu Ser
243         275                 280                 285
245 Lys Phe Arg Leu Thr Thr Lys Phe Phe Gly Thr Phe Leu Pro Glu Val
246 290                 295                 300                 305
248 Ala Lys Lys Phe Pro Asn Met Lys Ile Gln Ile His Val Ser Ala Ser
249             310                 315                 320
251 Thr Pro Pro His Leu Ser Val Gln Pro Thr Gly Leu Thr Phe Tyr Pro
252             325                 330                 335
254 Ala Val Asp Val Gln Ala Phe Ala Val Leu Pro Asn Ser Ser Leu Ala
255             340                 345                 350
257 Ser Leu Phe Leu Ile Gly Met His Thr Thr Gly Ser Met Glu Val Ser
258         355                 360                 365
260 Ala Glu Ser Asn Arg Leu Val Gly Glu Leu Lys Leu Asp Arg Leu Leu
261 370                 375                 380                 385
263 Leu Glu Leu Lys His Ser Asn Ile Gly Pro Phe Pro Val Glu Leu Leu
264             390                 395                 400
266 Gln Asp Ile Met Asn Tyr Ile Val Pro Ile Leu Val Leu Pro Arg Val
267             405                 410                 415
269 Asn Glu Lys Leu Gln Lys Gly Phe Pro Leu Pro Thr Pro Ala Arg Val
270             420                 425                 430
272 Gln Leu Tyr Asn Val Val Leu Gln Pro His Gln Asn Phe Leu Leu Phe
273         435                 440                 445
275 Gly Ala Asp Val Val Tyr Lys
276 450                 455
```

VERIFICATION SUMMARY   DATE: 05/23/2002
PATENT APPLICATION: **US/09/446,415B**   TIME: 17:01:32

Input Set : **A:\11034US02.SEQ.txt**
Output Set: **N:\CRF3\05232002\I446415B.raw**

L:184 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:2